```
GenCore version 5.11.3 Copyright (c) 1993 - 2003 Compugen Ltd
```

OM protein - protein search, using sw model

January 16, 2003, 16:30:12; Search time 16.8286 Seconds (Without alignments) 28 464 Million cell updates/sec

US-09-856-070-23 55 1 FLMLRLQDYEE 11 Title: Perfect score:

Scoring table: sedneuce:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues Searched:

Total number of hits satisfying chosen parameters:

112892

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing lirst 45 summaries

SwissProt\_40:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

4 1 2 2 2 2		are :					
NO.	Score	Match	Length	DB			
	- L. C.	100	OKR	: -	EZRI_ROVIN	P31975 bos taurus	
CA	in in	100.0	20 50 50	_	EZEL HUMAN	311 homo	
٣	52	94.5	585	-	EZR:_MOUSE		
4	36		886	-	RASU_SULAC	033600 sulfolobus	
Ŋ	36		715	-	PBS2_BPAPE	Q98sp7 brachydanio	
¥	46		2472	-	SPON_HUMAN	Olamia homo sapien	
7	36		2472	4	SPCN_RAT	ratte	
ထ	36		2477	-	SPCN_CHICK	P07751 gallus gall	
on	35		892		AAC1_HUMAN	P12814 homo sapien	
10	35		892		AAC1_RAT	Q971p2 rattus norv	
11	35		964	-	PLE1_MOUSE	_	
12	35		4473	-	PLE1_CRIGR	09)155 cricetulus	
13	35		4684	-	PLE1_HUMAN	015149 homo sapien	
14	35		4687	-	PLE1_PAT	P30427 rattus norv	
15	34	61.8	332	_	KC2A_MATRE		
16	34		333	_	KC21_AKATH		
17	34		333	-	KC22_ARATH		
18	34		333	~	KC23_ARATH	064817 arabidopsis	
19	34		365	-	ECT1_SCHPO		
()	3.4		387		YCH5_YUAST	253159 saccharomyc	
<u></u>	34		405	· ·	FUT4_HUMAN	222083 homo sapien	
C4	34		467		INVO_MOUSE		
23	34		544	1	THS_METTL		
77	34	£ .	741	- 1	RSG2_PFOME	Pliala drosophila	
C4 IU	77		୍ଞଞ	,· •	RASO_PYPAR		
26	34		978		RA50_AQUAR		
27	3.3		177		PUR6_CORAM	Q44679 corynobacte	
28	33		196		VITA_BP17		
9.	e e		57.5		YM?4_YEAST	205024 saccharomyc	
30			25A		YT98_MYCTH	Q10859 mycobacteri	
31	3.3		270	_	CWFG_SCHPO		
32	3.3		420	-	HILL HUMAN	PS4257 home sapies	
33	33	0.09	522	_	CPV1_ORENI	P70091 orecchromis	

P70194 mus musculu	Q21565 caenorhabdi	99bxc9 homo sapien	Q9cwi6 mus musculu	Q99mb9 rattus nory	P16591 homo sapien	P34703 caenorhabdi	P09603 homo sapien	F34548 caenorhabdi	P37599 bacillus su	Q9uy11 pyrococcus	OBren3 fusobacteri
KUCK_MOUSE	AMT3_CAPT1	BBS2_HUMAN	BBS2_MOUSE	PBS2_PAT	FER_HUMAN	EMB5_CAEEL	CSF1_HUMAN	SQV3_CAEEL	CHEV_BACSU	SYW_PYRAB	EX71FUSNN
_	_	٦	_	_	~4	<b></b>	_	-	-	П	-
548	ب د: ۲	721	721	151	822	1521	7. U	289	303	385	404
0.09	6.03	60.0	60.09	0.09	60.09						58.2
33	33	33	33	33	3.5	33	#: €:	Ç,	25	32	35

## ALIGNMENTS

	EXPLENDIN STANDARD; PRT; 580 AA. P31976. P31976. P31976. P31978. P31976. P31978. P31976. P31978. P31978. P31978. P31978. P31978. P3111. P31978. P31978. P31978. P31978. P31979. P31979
	1976. [1973] (Rel. 26, Created) -JUL-1993 (Rel. 26, Last sequence update) -JUL-1993 (Rel. 26, Last sequence update) -JUL-1993 (Rel. 26, Last annotation update) -JUL-1993 (Rel. 40, Last annotation update)
	-ULL-1993 (Rel. 24, Created) -ULL-1993 (Rel. 24, Created) -ULL-1993 (Rel. 26, Last sequence update) -ULL-1993 (Rel. 26, Last sequence update) -ULL-1993 (Rel. 26, Last sequence update) -ULL-1993 (Rel. 26, Last sequence) -ULL-1993 (Rel. 26, Last sequence) -ULL-1993 (Rel. 26, Last sequence) -ULL-1993 (Bovine) -ULL-1994 (Rel. 26, Letterload (Creation) -ULL-1994 (Rel. 26, Letterload (Creation) -ULL-1995 (Rel. 26, Letterload (Letterload (Le
	July 1973 (Rel. 40). Last sequence update) July (Rel. 40). Last annotation update) July (Rel. 40). Last annotation update) July (Cytovillin) (Villin 2). July (Bovine).  Activity, Medava, Cherdata; Cramata, Vertebrata; Euteleostomi; Activity, Medava, Cherdata; Cramata, Vertebrata; Bovoidea; July (Bovinec, Hos. July (Bovinec, Hos. July (Bovinec, Hos.) July (Bovinec, Hos.) July (Bovoidea; Bovoidea; Bovoidea; Bovoidea; July (Bovoidea; Bovoidea; Bovoidea; Bovoidea; Bovoidea; July (Bovoidea; Bovoidea; Bovoi
	rin (pil) (Cytovillin) (Villin 2).  22.  23.  24.  25.  26.  27.  27.  28.  28.  28.  28.  29.  29.  29.  29
	Sturus (Bovine).  Sturus (Bovine).  Status (Bovine).  Madydta, Mataboa, Chordata: Cranata, Vertebrata; Euteleustomi;  malia; Eutheria; Gearlindariyla; Ruminaniia; Pecora; Bovoidea;  sidac, Bovinac, Hos.  JITAXID=9913;  JUENCE FROM N.A.  SSUE-Brain;  SSUE-Brain;  A. Zhao H., Saijch F., Duman P.S., Nestler E.J.;  Arin and ostconcrtin, two proteins associated with ceil shape and  with, are enriched in the locus coeruleus.";  JUENCE OF 1-15 AND 126-140.  JUENCE OF 1-15 AND 126-140.
	s taurus (Bovine).  Argida, Metadoa, Chordata; Cianata, Vertebrata; Euteleostomi; Argida, Metadoa, Chordata; Cianata, Vertebrata; Euteleostomi; Judac, Bovinac, Hos.  AllaxiD=9913; JUENCE FROM N.A.  SSUEBrain; AllaxiD=8913; AllaxiD=8913; AllaxiD=9913; AllaxiD=9913; AllaxiD=9913; AllaxiD=9913; AllaxiD=9913; AllaxiD=1000
	<pre>ABCOVED. Metaloda Chordata: Clatuata. Vertebrata: Enteleustomi; maila; Eutheria; Cerartiodactyla; Ruminantia; Pecora; Bovoidea; didae, Bovinae, Hos.  ## [TaxID=9913; didae, Box M.A.  SSDE-Brain; crison C M. Zhon H., Saijoh K., Puman P.S., Nestler E.J.; crison C M. Zhon H., Saijoh K., Puman P.S., Nestler E.J.; crison C M. Zhon H., Saijoh K., Puman P.S., Nestler E.J.; crison C M. Zhon H., Saijoh K., Puman P.S., Nestler E.J.; crison C M. Zhon H., Saijoh K., Puman P.S., Nestler E.J.; crison C M. Zhon H., Saijoh K., Puman P.S., Nestler E.J.; argin and ostconcrin, two proteins associated with cell shape and pwth, are enriched in the locus coeruleus."; din and ostconcrin, two proteins associated with cell shape and pwth, are enriched in the locus coeruleus."; din and ostconcrin, two proteins associated with cell shape and crison E.Z. Januaria. din and ostconcrin, two proteins associated with cell shape and crison E.Z. Januaria. din and ostconcrin, two proteins associated with cell shape and crison E.Z. Januaria. din and ostconcrin, two proteins associated with cell shape and crison E.Z. Januaria. din and ostconcrin, two proteins associated with cell shape and crison E.Z. Januaria. din and ostconcrin, two proteins associated with cell shape and control of the locus coeruleus."; din and ostconcrin, two proteins associated with cell shape and control of the locus coeruleus."; din and ostconcrin, two proteins associated with cell shape and control of the locus coeruleus."; din and ostconcrin, two proteins associated with cell shape and control of the locus coeruleus."; din and ostconcrin, two proteins associated with cell shape and control of the locus coeruleus."; din and cell shape and cell</pre>
	ministration by the contraction of the contraction
	Jidae, BoVliac, Hos.  JiaxID=9913;  JIENCE FROM N.A.  SSUE=Brain,  SSUE-Brain,  And Ostconertin, two proteins associated with ceil shape and  wth, are enriched in the locus coeruleus.";  Cell. Neurosci. 4:64-73(1993).  PIENCE OF 1-15 AND 126-140.  SSUE-Kidney.
	1laxiD=9913; 20ENCE FROM N.A. SSUB-Brain; SSUB-Brain; F. Zhao H , Saijoh F , Duman P S Nestler E.J.; Frin and ostconcrtin, two proteins associated with ceil shape and bowth, are enriched in the locus coeruleus."; F. Ceil. Neurosci. 4:64-73(1993). Discrete of 1-15 AND 126-140. SSUB-Kidney.
	JENCE FROM N.A. SSUE-Brain; SSUE-Brain; C M, Zhao H, Saijoh F, Duman P S., Nestler E.J.; Arison C M, Zhao H, Saijoh F, Duman P S., Nestler E.J.; Arrin and ostronoctin, two proteins associated with cell shape and DWth, are enriched in the locus coeruleus."; I. Cell. Neurosci. 4:64-73(1993). GUENCE OF 1-15 AND 126-140. SSUE-Kidney.
	JOHNEE FROM N.A.  SUSSEPERAIN  Typen C M., Zhao H., Saijoh K., Duman P S., Nestler E.J.;  Typen C M., Zhao H., Saijoh K., Duman P S., Nestler E.J.;  Arin and ostroncetin, two proteins associated with ceil shape and  Owth, are enriched in the locus coeruleus.";  1. Ceil. Neurosci. 4:64-73(1993).  JUENTE OF 1-15 AND 126-140.  SSUE-Kidney.  in Neurosci.77. Duhwed-R660651.
	The state of the s
PA Re	arin and ostconectin, two proteins associated with ceil shape and with are enriched in the locus coeruleus."; 1. Ceil. Neurosci. 4:64-73(1993). 20ENCE OF 1-15 AND 126-140. SSUE-Kidney.
	Dwth, are enriched in the locus coeruleus."; 1. Cell. Neurosci. 4:64-73(1993). 20ENCE OF 1-15 AND 126-140. SSUE-Kidney.
	1. Cell. Neurosci. 4:64-73(1993). prener of 1-15 AND 126-140. stubentagiat. buthmed-#660651.
	] 
	20ENCE OF 1-15 AND 126-140. SSUE-Kidney. in N=4K53€737. bubbmed+866Ω651.
RP SE	SSUE=Kidney; iint=Gk23Gi37: buhmmd=Bk60651.
	21 1 N 1 = Q 6 2 3 Q 1 4 7 7 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
	STATES OF STATES TO SECOND STATES STA
	lat A., Gorbad M.C., Bouet F., Riviere S.;
	roteins and their amino acid compositions: uniqueness, variability,
P.T. an	and applications.";
	ch. Biochem. Biophys. 330:229-237(1996).
	- FUNCTION: PROBABLY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL
	STRUCTURES TO THE PLASMA MEMBRANE.
ال	
	- SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN.
	This SWISS-PROT entry is copyright. It is produced through a collaboration
74 22	tween the Swiss institute of Bioinformaties and the IMML outstation
	s European Bioinformatics Institute. There are no restrictions on i
	s by non-prolit institutions as long as its content is in no wa
	diffed and this statement is not removed. Usage by and for commercia
	entities requires a license agreement (See http://www.isb-sib.ch/announce/
	send an emain to incense@isb-sib.ch).
DO	
	кмы, м98498; даазо510.1;
	Lerbro; IPRUG0299; Band_4.1.
된	Enterproj Iren00708, Ez/rad/moesin.
	am; PF00373; Band_41; 1.
	аш.) РЕОО769, ЕКМ. 1.
H-1	INTS: PP00935; HAND41.
DR SM	SMART; SMU0295; H41; 1.
	DSITE: PS00660: BAND 41 1; 1.
	DSITE: FS00661; BAND 41 2; 1.
	PROSITE: PS50057: BAND 41 3: 1.
	actural protein. Ortoskoleton, Phosphorylation.
N - 1.4	(1) (1) (1) (1) (1) (1) (1) (1) (1) (1)

```
"Identification of earin as an 81 kDa tyrosine phosphorylated protein
                                                                                                                                                        Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Purunen O., Wingvist R., Pakkanen R., Grzeschik K.H., Wahlstroem T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIJNE-96311348; PubMed-8713105;
Eqerton M., Moritz K.L., Druker B., Kelso A., Simpson R.J.;
"Identilication of the 70kD heaf shock cognate protein (Hsc70) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alpha-actinin Las novel phosphotyrosine-containing proteins in T
lymphorytes.":
                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota, Metazoa, Cherdata, Craniata, Vertebrata, Euteleostemi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Offenwaelder B., Obermaier B., Mewes H.-W., Weil B., Wiemann S.:
Submitted (MAR 2000) to the EMBL/GenBack/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification of the two major epidermal growth factor-induced
                                                                                                                                                      ò
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tyrosine phosphorylation sites in the microvillar core protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Egerton M., Burgess W.H., Chen D., Druker B.J., Bretscher A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cyrovillin, a microvillar Mr 75,000 protein, cDNA sequence, prokaryotic expression, and chromosomal localization."; J. Biol. Chem. 264:16727-16732(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gould K.L., Bretschet A., Esch F.S., Hunter T.,
"cDNA cloning and sequencing of the protein-tyrosine kinase
substrate, errin, reveals Remelegy to band 4.1.";
                                                                                                                100.0%; Score 55; DB 1; Length 580; 100.0%; Pred. No. 0.005;
                                                                                                                                                    0, Indels
              PHOSPHORYLATION (BY PDGFR) (BY SIMILARITY).
                                                  PHOSPHORYLATION (BY PUGER)
                                                                                    ECD663E5C200FAA3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biochem. Biophys. Pes. Commun. 224:666-674(1996).
                                                                                                                                                                                                                                                                                                       EZRI_HUMAN STANDARD, PRT; 585 AA P15411; P24714; Q9NSJ4; O1-AVF-1990 (Rel. 14, Created) (NOV-1991 (Rel. 20, Last sequence update) 15-UNN-2002 (Rel. 41, Last annotation update) (Errin (PRI) (Cytovillin) (VIIIn 2).
                                                                (BY SIMILARITY)
                                                                                                                                                    S, Mishatches
BAND 4.1-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEGUENCE FROM N.A., AND PARTIAL SEQUENCE.
MEDLINE-90076135; PubMed-2591371;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 267:19258 19265(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FISSUE-Placenta;
MEDLINE-89380299; PubMed-2674140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-92406868; PubMed-1382070;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-92488649; PubMed-1381489;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 171-179 AND 342-349.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in T cells.";
J. Immunol. 149:1847-1852(1992).
                                                                                  68629 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBO J. 8:4133-4142(1989).
                                                                                                                                                    Conscrivative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION BY PDGFR
                                                353
                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
                                                                                                                                                                                                                   345 ELMURIQDYEE 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kried J., Hunter T.;
                                                                                                                                                                                      1 ELMLRLQDYRE 11
                                                                                580 AA:
                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBL_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Same Ison L.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Vaheri A.;
                                                                                SEQUENCE
                                                                                                                  Query Match
                                                                                                                                    Local
                MOD_RES
                                                  MOD_RES
NIVWOR
                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                         ttere?
```

```
between the Swiss Institute of High formaties and the EMH, outstation the European Bioinformatics Institute There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                        This SWISS-PROI entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GdbS
FUNCTION: PROBBELY INVOLVED IN CONNECTIONS OF MAJOR CYTOSKELETAL. STRUCTURES TO THE PLASMA MEMBRANE. SUBCELLULAR LOCATION: MICROVILLAR PERIPHERAL MEMHRANE PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-92064635; PubMed-1955455; Fundyama N., Nagatuchi A., Sato N., Tsukita S., Tsukita S.; Fundyama N., Nagatuchi A., Sato N., Tsukita S., Tsukita S.; "Radixin is a novel member of the band 4.1 family."; J. Cell Biol, 115:1039-1048(1991).
-i. Function: PROBABRY NOWINED IN CONNECTIONS OF MAJOR CYTOSKELETAL. STRUCTURES TO THE PLASMA MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciuroqnathi, Muridae, Murinae, Mus.
                                                                        TISSUE SPECIFICITY: COMPONENT OF THE MICROVILLE OF INTESTINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .
O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 55; DB 1; Length 585; 100.0%; Pred. No. 0.0051; Didcts 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION (BY PDGFR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION (BY PDGFR).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2A8440140E3B06CC CRC64;
                                                                                                         PIM: PHOSPHORYLATED BY PROTEIN-TYROSINE KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE: PS00660: BAND.41_1: 1.
PROSITE: PS00661: BAND.41_2: 1.
PROSITE: PS50057: BAND.41_3: 1.
Structural protein, Cytoskeleton, Phosphorylation.
INIT.MET
                                                                                                                         SIMILARITY: CONTAINS 1 BAND 4.1-LIKE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-1992 (Rel. 22, Created)
01 MAY-1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   V -> L (IN REF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BAND 4.1-LIKE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          !* SUBCELLULAR LOCALION: Cytoplasmic.
                                                                                                                                                                                                                                                                                                                                 EMBL; AL162086; CAB82418.1; ALT_INIT.
PIR; S09263; S09263.
PIR; A34400; A34400.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Earin (p81) (Cytóvillín) (Villin 2).
                                                                                                                                                                                                                                                                                                                 EMBL; J05021; AAA51278.1; ALT_INIT
                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000299; Band_4.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                585 AA; 69267 MW;
                                                                                                                                                                                                                                                                                                                                                                                      SWISS-ZDPAGE; P15311; HUMAN.
                                                                                                                                                                                                                                                                                                 EMBL; X51521; CAA35893.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00373; Band_41; 1.
Pfam; PF00769; ERM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00935; BAND41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIANDARD;
                                                                                                                                                                                                                                                                                                                                                                                               Gesew, HGNC.12691, VILZ.
MIM, 123900, -.
                                                    (CYTOPLASMIC SIDE)
                                                                                         EPITHELIAL CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                         interPro, IPR000798,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       345 ELMLRLQDYEE 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ELMLRLQDYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EZRI_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFILICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P26040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EZRI_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VIL2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     qq
```

```
This SWISS-PROT entry is capyright. It is produced through a collaboration between the Swiss institute of Bioinformatics and the EMBL outstation the Brucopean Bloinformatics lastitute. There are no restrictions on its use, by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www_isb-sib_ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Blie C., Baucher M.F., Fondrat C., Forterre P., Marmeter proteins in the "A protein related to eucaryal and bacterial DNA-meter proteins in the hyperthermophilic archaeon sullalobus acidecaldaric.", J. Mol. Evol. 45.107-114(1997).
-i. FUNCTION: Involved in DNA doublerstrand break repair (DSBF). The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              radsO/mrell complex passesses single strand endulusiease activity and Alf dependent double strand specific executions and affile the description of provides an AIP-dependent countrol of micil by unwinding and/or repositioning tNA ends into the mirell active site (R)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
TISSUR SPECIFICITY: COMPONENT OF THE MICROVILLE OF INTESTINAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBUNIT: Forms a complex with mrell (By similarity).
-!- SIMILAPITY: RELONGS TO THE SMC FAMILY, RAD50 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94.5%, Score 52, DB 1, Length 585, 90 9%; Pred No 0 019;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C, indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PHOSPHORYLATION (BY PEGFP) (BY SIMILARITY).
PHOSPHORYLATION (RY PIGER)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2057EDELELBOOSDI CRC64;
                                                         -i- FIM: PHOSPHORYLAIED BY PROIEIN-TYROSINE KINASES-i- SIMILARITY: CONTAINS I BAND 4.1-LIKE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Structural protein, Cytoskeleton, Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-001-2001 (hel. 40, last sequence update)
16-001-2001 (Hel. 40, last annotation update)
DNA double-strand break repair rad50 ATPase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            i, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BAND 4.1-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STPAIN ALCO (4.654), MOTH (1775), DSM EAG, MEDLINE-97362314; Pubmed-9211741;
                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR: B41129; B41129.
MGD; Mil:98931; Vil2.
InterPro; IPP000249; Rand_4 1.
InterPro; IPR000798; Ez/rad/moesin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE: PS00660; BAND 41_1; 1. PROSITE; PS00661; BAND 41_2; 1. PROSITE; PS50057; HAND 41_3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   585 AA: 69214 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X60671; CAA43086.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00373; Band_41; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sulfolobus acidocaldarius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDAPD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00935; BAND41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   353
                                 EPITHELIAL CELLS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00295; B41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         345 ELMLRLQDYEQ 355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ELMLRLQDYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PF00769; ERM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
es 10, Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCB1_Tax1D-2285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    57
145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PASO_SHLAC
Ossboū;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sulfolobus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INIT_MET
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PAD50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOUTH THE THE TENENCE OF THE PERSON OF THE P
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the IMML outstation-the European Proinformatics institute. There are no restrictions on its use by non-profil institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial or send an email to license@isb-sib.ch).
                                  between the Swiss institute of Bioinformatics and the EMBL outstation - The European Bioinformatics Institute. There are no restrictions on its mast by non-pool; institutions as long as its content is in no way modified and this strengthent is not removed. Usage by and for commercial entities requires a license agreement (See http://www.ish.ch/announce/or send an email to license*isb.ch).
SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIJNIC-21181710: PebMcd-11285252;
MEDIJNIC-21181710: PebMcd-11285252;
MEDIJNIC-21181710: Pearly C. C. Carmi R., Elbedour K., Van Maldernem L., Nishimura D.Y., Saarky C.C., Carmi R., Elbedour K., Van Maldernem L., Fullons B., Taum R., Pavalla R. E., Widderski R. E., Bragge K. E., Haider N.B., Arinek-Biack A.E., Ying L., Duhl D.M., Gorman S.M., Heon E., Jannaccone A., Bonneau B., Bieseeker i.G., Jacobson S.G., Stone E.M., Sheffield V.C.,

"Positional cloning of a nevel gene on chromosome 16g causing Bardet-Biedl syndiome (BBS2).",

Hum Mol. Genel 10-8K5-874(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Actinopteryqii; Neopteryqii; Leleostel; Ostariophysi; Cyprinilormes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70.9%; Score 39; DB 1; Length 886; 63.6%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            65.5%, Score 36; DB 1; Length 715; 70.0%; Pred. No. 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21.00
                                                                                                                                                                                                                                                                                                                                                                                                                        Promis Puckets, sec_s, promise protons; Prodouble prodouble prodouble produced by Prodouble produced by Prodouble produced by Produced produced by Produced By 37 ATP (BY SIMILARIY).

DOMAIN 174 727 COLLED COLL (POTENTAL).

SEQUEN'E HAS AA: 10.657 MW 0.000AE193194104 CROS4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -
7: 326770A945834m96 mp0647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last Sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Bardet Biedl syndrome 2 protein homolog.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Brachydanio retio (Sebrafish) (Danio tetio).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prod. No. 30:
2, Mismatobas
                                                                                                                                                                                                                                                                                                                                Interpro: IPR003439; ABC_transportr.
Interpro: IPR003395; SMC_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF342739; AAK28555.1; -. SEQUENTE 715 AA; 79125 MW;
                                                                                                                                                                                                                                                                                              EMPL: Y10687; CAA71688.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservation Con
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 63.6
Matches 7: Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF02463; SMC_N;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   259 FIALRIKDPFE 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ELMLRLQDYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Most Todal Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          348 LMLELRNYEE 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 LMLFLQDYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HHS2_BRARE
098SP7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BRS2_RRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HBS2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SET TENT TO SECUL OF THE SECURITY OF THE SECURITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ò
```

```
498
737
1586
                                                                                                                                                                                                                                                                                                                                                                                                                                 149
255
361
467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              573
678
784
890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2091
                                                                                                                                                                                                                 MIM; 182810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEPEAT
CA_BIND
CA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VAPIANT
                                                                                                                                                                                                      Genew;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SITE
"Generation of diversity in nonerythroid spectrins. Multiple polypebildes are predicted by sequence analysis of cDNAs encompassing the coding region of human momerythroid alpha-spectrin."; J. Hiol. Chem. 265:4427-4434(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murakami N., Speed W.C., Seaman M.I., Zychowski R., Werterberg L., Pakstis A.J., Kidd J.P., Kidd K.K.; "Association and linkage analyses of the nonerythroid alpha-spwortrin (SPTAN) gene on chromosome 9434 with a large Swedish kindred.", Submitted (MAY-1999) to the FMHJ/Genhank/DDRI databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "cDNA cloning, sequencing and chromosome mapping of a non-erythroid spectrin, human alpha-todrin.";
Differentiation 34:68-78(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                          McMahon A.P., Giebelhaus D.H., Champion J.E., Railes J.A., Lacey S.
Carritt B., Henchman S.K., Moon R.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: FOURIN, WHICH SEEMS TO BE INVOLVED IN SECRETION, INTERACTS WITH CALMODILIN IN A CALCTUM-DEPENDENT MANNER AND IS THUS CANDIDATE FOR THE CALCIM-DEPENDENT MOVEMENT OF THE CYTOSKELETON AT THE MEMBRANG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHRINITY TIKE FRYTHROMYTE SPECTEIN, THE SUPCTEINS ARE CAPABLE TO FORM DIMPRS WHICH CAN FURTHER ASSOCIATE TO
                       01881s; Ulf6606; O9P00V0; Ul4186; Ulanov 1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
Spectrin alpha chain, brain (Spectrin, non-erythroid alpha chain)
64pha-11 spectrin) (Fodrin alpha chain)
                                                                                                                                                                                                                                                                                            "Complete cDNA sequence of human alpha II fetal brain spectrin.";
Submitted (FEB-1997) to the EMBL/GenHack/GDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 811-1529 FROM N.A., VARIANT ILE-1300, AND MUTAGENESIS
                                                                                                                      Eukaryolu, Metazoa, Chordata, Graniata, Vertebrata, Euteleostomi,
Mammalia: Eutheria: Primates; Catarrhini, Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McMahon A.P., Giebelhaus D.H., Champion J.E., Railes J.A., Lacey
Carritt B., Henchman S.K., Moon R.T.;
Differentiation 34:241-241(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stabach P.R., Cianci C.D., Glantz S.B., Zhang Z., Morrow J.S., "Site-directed mutagenesis of alpha II spectrin at codon 1175 modulates its mu-calpain susceptibility.":
                                                                                                                                                                                                                                                                                                                                                               McMahon A.P., Moon R.T.;
"Structure and evolution of a non-erythroid spectrin, buman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIMILARITY: BELONGS TO THE SPECTRIN FAMILY. SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS
                   PRT; 2472 AA
                                                                                                                                                                                                                                                                                                                                                                                               Riochem, Soc. Trans. 15:804-807(1987)
                                                                                                                                                                              MEDILINE-90170948; PubMed-2307671;
                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-87277023; PubMed-3038643;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WEDLINE-97146462; PubMed-8993318;
                                                                                                                                                                                                                                                                                                                                                   MEDLINE-88083942; PubMcd-3691949;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1073-1349 FROM N A
                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 676-1595 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 676-1595 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diochemistry 46:57-65(1997).
                                                                                                                                                                                                                                                                     TISSUE-Fetal brain;
Clanci C.D., Morrow J.S.;
                   STANDARD;
                                                                                                                                                                                         Moon R.T., McMahon A.P.;
                                                                                                            Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rissue-Fetal brain;
                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                           NCBI_TaxID-9606;
                                                                                                SPIANI OR SPIA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TETTRAMERS.
                                                                                                                                                                                                                                                                                                                                                                                  alpha-fodrin.
                                                                                                                                                                                                                                                                                                                                         TISSUE-Lund;
                    SPCN_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ERRATUM.
        SPCN_HUMAN
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Micinformatics and the EMH, outstation the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial cuttics requires a literate agreement (Such that, //www.isb-sib.ch/announce/or sond an email to licensealsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00018; EF_HAND; 1.
PROSITE; PS500018; EF_HAND; 1.
PROSITE; PS50002; SH3; 1.
PROSITE; PS50002; SH3; 1.
Capping protein; Calmodulin binding; Repeat, SH3 domain, Polymorphism.
REPEAT 10 42
SPECTRIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q -> QLSKLL (IN REF. 2).
F -> R (IN REF. 3 AND 4).
N -> S (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLEAVAGE (BY MU-CALPAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N \rightarrow K \text{ (IN REF. 2)}.

F \rightarrow S \text{ (IN REF. 2)}.

V \rightarrow I \text{ (IN REF. 2)}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IA -> FD (IN REF. 2).
A -> D (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /FT1d-VAR_012227.
SIMILARITY: CONTAINS 1 SH3 DOMAIN.
SIMILARITY: CONTAINS 23 SPECTRIN REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECTRIN 11.
SPECTRIN 12.
SPECTRIN 13.
SPECTRIN 14.
SPECTRIN 15.
SPECTRIN 16.
SPECTRIN 16.
SPECTRIN 19.
SPECTRIN 19.
SPECTRIN 19.
SPECTRIN 19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECTRIN 2.
SPECTRIN 3.
SPECTRIN 4.
SPECTRIN 5.
SPECTRIN 5.
SPECTRIN 6.
SPECTRIN 7.
SPECTRIN 9.
SPECTRIN 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIRIN 22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPECTRIN 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPECTRIN 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EF-HAND 1
EF-HAND 2
                                                                                                                                                                                                                                                           EMBL, U83867, AD541498.1, ...
EMBL, M24773, AAA52468.1, ...
EMBL; M18627, AAA51702.1, ...
EMBL; U26396, AAB5U364.1, ...
EMBL; AP148808, AAF26672.1, ...
HSSP, P07751, 1AEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro, IPR002017; Spectrin.
Pfam: PF00018; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protom; Pu000012; EF-hand; 1. Protom; Pu000066; SH3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002048; EF-hand.
InterPro; IPR001452; SH3.
                                                                                                                                                                                                                                         EMBL; J05243; AAA51790.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00036; ethand; 4.
Pfam; PF00435; spectrin; 32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00452; SH3DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                           HGNC:11273; SPTAN1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00054; EFb; 2.
SMART; SM00326; SH3; 1.
SMART; SM00150; SPEC; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1026
1089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2195
2310
2347
2390
1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 656
762
868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1974
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    between the Swiss Institute of Ricinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for communications requires a license agreement (See http://www.ish-sit.ch/announce/
                                                                                                   Ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        33ps
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryona: Metazoa; Chordata; Craniata; Vertebrata; Euteleosiomi;
Mammalia; Eutheria; Podentia; Sciurognathi; Muridae; Murinae; Pattus
                                                                                                                                                                                                                                                                      15. Jun. 2002 (Rel. 41, List acqueace updite)
Spectrin alpha chain, brain (Spectrin, non-crythroid alpha chain)
(Alpha-II spectrin) (Fodrin alpha chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Wistar; TISSUE-Liver;
Kalamaraki P., Gazzotti P.;
"Structural and functional characterization of the calmodulin and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N A TISSUE-SKeletal muscle; Should, write the T.Y. Pandall W P., Rhoch P T.; Zhou D., Wrstitl J.A., Porter N C., Pandall W P., Rhoch P T.; Expressional cloudy of alpha-fodiin from rat skeletal muscle."; Submitted (AUG-1998) to the EMBL/Genhank/DDBJ databases.
                                                                                                c
                                                               Match 65.5%, Score 36, DB 1; Longth 2472; Local Similarity 63.6%; Fred No 1.20+07; Local Similarity 63.6%; Rismatches 2; Indels les
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 2 EP-HAND CALCIUM-BINDING DOMAINS. SIMILARITY: CONTAINS 1 SH3 DOMAIN. SIMILARITY: CONTAINS 23 SPECIFIN MERPEATS.
                                                                         Ja ...
2010;
-1 Indels
2347 2348 DG > EF (IN PEF, 2).
2448 2448 I -> Y (IN PEF, 2).
2472 AA; 284279 MW; CDATGF4462A7028D CMC61.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             calpain binding domains of rat liver alphail spectrin."; Submitted (ARS 1996) to the PMPI Jernank/APRI Jatabases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE SPECTRIN FAMILY. SIMILARITY: CONTAINS 2 RF-HAND CALCUMAN NAME.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or send an email to licensewish-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IISSUE-Kidney;
MEDLINE-89327227; PthMed-2753883;
                                                                                                                                                                                                                                                        P160<u>B</u>6, P70477: 088663;
01-APR 1990 (Rel. 14, Creared)
15-IIN-2002 (Rel. 41, List soqu
15-JUN-2002 (Rel. 41, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1292 2321 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AF084186; AAC33127[1; -. EMBL; J04828; AAA40770.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro: IPRO02048: EF-hand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBI.; X90845; CAA62350.1;
                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Kat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIR; A32612; A32612.
HSSP; P07751; IA.T3.
                                                                                                                                                                 970 ELVLALYDYQE 980
                                                                                                                                1 FLMLRLQOYEP 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                NCB1_1axID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TETRAMERS.
                                  SPORPNOR
                                                                                                                                                                                                                                                 SPCN_PAT
   CONFLICT
                    CONFLICT
                                                                  Query Match
                                                                                                   Matches
                                                                                                                                                                                                                 RESULT 7
                                                                                                                                                                                                                                  SPCN_KAL
                                                                                    Best
                                                                                                                                                                                                                                                οy
```

```
HADFG_EHNRSH (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gallus qallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria, Aves, Neognathae, Galliformes, Phasiauidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Four-2010 (Rel. 19, Last Sequence update)
Spectrin alpha chain, brain (Spectrin, non crythroid alpha chain)
(Fodrin alpha chain).
                                                                                                                                                                                                                                                                                                                                                                                                                                        Scotte 36, DB 1, Length 2472;
Pred. No. 1.20+02;
2: Mismatches 2, Indela
                                                                          PROSTIE: PS00018: EF HAND: 2.
PROSTIE: PS50002; SH3: 1.
Cytoskeleton: Membrane: Calmodulin-binding: Actin-binding:
                                                                                                                                                                                                                                                                                                                                                                                                                         UBDDFU1A2871278A CRC64;
                                                                                                       Capping protein; Calcium-binding; Repeat; SH3 domain. REPEAT 1. 42
                                                                                                                                                                                                                                                                                                                   STACTER 21.
SPECTRIN 22.
SPECTRIN 23.
EF-HAND 1 (POTENTIAL).
EF-HAND 2 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                 D -> Y (IN REF. 3).
V -> L (IN REF. 1).
L -> A (IN REF. 3).
KL > NV (IN REF. 1).
KL > NV (IN REF. 1).
QQQQANITSVI → HADF6VE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPT; 2477 AA.
                                                                                                                                                                                                                    SPECTRIN 11.
SPECTRIN 12.
SPECTRIN 13.
SPECTRIN 14.
SUPCCIPIN 15.
SPECTRIN 15.
SPECTRIN 18.
SPECTRIN 18.
SPECTRIN 18.
SPECTRIN 19.
SPECTRIN 19.
                                                                                                                                                                                SPECTRIN 9.
SPECTRIN 9.
SPECTRIN 10.
                                                                                                                         SPECTRIN 2.
SPECTRIN 3.
SPECTRIN 4.
SPECTRIN 5.
                                                                                                                                                              SPECTRIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE 89093238; PubMed 2910879;
                                                                                                                                                                                                                                                                                                                                                                                                                         LB4635 MW;
LiterFig. IPPS01452, SH3.
InterPro, IPR02017, Spectrin.
Pfum, PF00018, SH3, 1.
Pfam, PF00018, SH3, 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00435; spectrin; 33.
SMAFT, SMC0054, ETE, 2.
SMART, SMC0326; SH3; 1.
SMART; SMC0150; SPEC; 29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD:
                                                                                                                                                                                                            1026
                                                                                                                                                                                                                      1089
1161
1231
                                                                                                                                                                                                                                                  1337
1443
1549
                                                                                                                                                                                                                                                                              1656
                                                                                                                                                                                                                                                                                                                    23 20 23 20 23 24 27 23 24 27
                                                                                                                                                                                                                                                                                                          1974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   970 ELVLALYDYOF 980
                                                                                                                                                                                                                                                                                                                                                                                                                2330 23
2472 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ELMLRLODYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Best Local Similarity
Matches 7; Cossery
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCB1_Tax1D=9031;
                                                                                                                                                                                                                                                                              1551
1658
1764
1870
                                                                                                                                                                                                                                                                                                                                                                  $29
                                                                                                                                                                                                            296
                                                                                                                                                                                                                               1091
                                                                                                                                                                                                                                                                                                                             2091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPCN_CHICK
                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                   REPEAT
REPEAT
REPEAT
CA_BIND
                                                                                                                                                                                                                                                                                                                                                                   CONFILCI
                                                                                                                                                                                                                                                                                                                                                                           CONFILCT
                                                                                                                                                                                                                                                                             REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                               REPEAT
REPEAT
                                                                                                                                 REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                            DOMAIN
KEPEAI
                                                                                                                                                                                REPEAT
REPEAT
                                                                                                                                                                                                                               REPEAT
REPEAT
                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus
                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                  KEPEAT
                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SPCN_CHICK
```

```
MEDLINE-98363217; PubMed-9699637;
Martinez J.C., Pisabarro M.E., Serrano L.;
"Obligatory steps in protein folding and the conformational diversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (4) MIDDLE DOMAIN (M),

(4) DOMAIN BETWEEN THE MIDDLE AND C-TERMINAL DOMAIN (MC),

(5) C TERMINAL DOMAIN (C).

NA AND WE DOMAINS ARE COMPOSED OF TYPICAL SPECTRIN 106 RESIDUES

REPEATS (1-8 POR MAND 12-19 FOR MC) AND ARE HOMOLOGOUS TO EACH

OTHER, N, M, AND C DOMAINS ARE COMPOSED OF SEQUENCES THAT DO NOT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRUCTURE HY NMR OF 2320-2403, MEDLINE-96067121; PubMed-7588621; Trave G., Lacombe J.-P., Pithl M., Saraste M., Pastore A.; "Molecular mechanism of the calcium-induced conformational change in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PUNCTION: MORPHOLOGICALLY, SPECTRIN-LIKE PROTFINS APPRAPING NE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: LIKE ERYTHROCYTE SPECTRIN, THE SPECTRIN-LIKE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wasenius V.-M., Saraste M., Knowles J., Virtanen I., Lehto V.-P., "Sequencing of the chicken non-erythroid spectrin cDNA reveals an intental repetitive structure homologous to the human crythrocyte spectrin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RELATED TO SPECTRIN, SHOWING A FLEXIBLE ROD-LIKE STRUCTURE.
THEY CAN HIND ACTIN BUT SEEM TO DIFFER IN THEIR CALMODULIN-
BINDING ACTIVITY. IN NOBERTHROLD TISSUES, SPECTRINS, IN
ASSOCIATION WITH SAME OTHER PROTEINS MAY PLAY AN IMPOPTANT
ROLE IN MEMBRANE OFGANIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARE CAPABLE TO FORM DIMERS WHICH CAN FURTHER ASSOCIATE TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (2) DOMAIN BETWEEN THE N-TERMINAL AND MIDDLE DOMAIN (NM),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-93063299; PubMod-1279444; Minarchia A., Noble M., Pauptit R., Wierenga R., Saraste M.; "CTystal structure of a Ste-homology 3 (SH3) domain."; Nature 359:851-855(1992).
Wasenius V.-M., Saraste M., Salven P., Eraemaa M., Holm M., Lehto V.-P.,
                                                                                                                                                                                                                                                             Masenius V.-M., Saraste M., Salven P., Braemaa M., Holm L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRUCTURE BY NMR OF 1763-1872.
MEDLINE-98022917; PubMed-9356261;
Pascual J., Pfuli M., Walther D., Saraste M., Nilges M.;
"Solution structure of the spectrin repeat: a left-handed antiparallel triple-helical coiled-coil.";
J. Mol. Biol. 273:740-751(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMAIN: SPECTRIN-LIKE PROTEINS HAVE FIVE DOMAINS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (1 R ANGSTROMS) OF 965-1025
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-KAY CPYSTALLOGPAPHY (2.0 ANGSTROMS) OF 969-1025
                                                                                          "Primary structure of the brain alpha-spectrin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FORM TYPICAL SPECIRIN REPEATS.
SIMILARITY: HELONGS TO THE SPECTRIN FAMILY.
SIMILARITY: CONTAINS I SHY DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nat. Struct. Biol 5-721-729(1998)
                                                                                                                                                                                                                                                                                                                                      Cell Biol, 108:1177-1178(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                   SECUDNCE OF 1695-2153 FROM N.A.
MEDLINE-85284928; FabMed 4029118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (1) N'TERMINAL DOMAIN (N),
                                                                                                                                Cell Hiol. 108:79-93(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14:4922-4931(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBO J. 4:1425-1440(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the transition state.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           he spectrin EF-hands.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LEPRAMERS.
                                                                                                                                                                                                                                                                                                        Lehto V. P.;
                                                                                                                                                                                                                      REVISIONS.
```

This SWISS PROT entry is copyright. It is produced through a collaboration between the SWISS Institute of Bioinformatics and the EMBL outstation. The European Holomormatics institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified as statement is not removed. Usage by and for connected entities requires a license aureement (See http://www.isb-sib.ch.) or send an email to licensee(isb-sib.ch).

1 ELMLRLQDYEE 11

ô

```
Caps
                                                                                                                                                                                                       Capping protein, Calcium-binding, Repeat; SH3 domain; 3D-structure, DOMAIN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ć
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65.5%; Score 46; DB 1; Longth 2477; 63.6%; Pred. No. 1.2c+02; Cive 2; Mismatches 2; Indels
                                                                                                                                                       SMART: SM00054; FFh; 2.
SMART: SM00156; SH3; 1.
SMART: SM00150; SPEC; 20.
PROSITE: PS00012; EHMD; 2.
PROSITE: PS50002; SH3; 1.
Cytoskeleton; Membrane; Calmodulin-binding; Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          285361 MW; AD4C876994E6AB49 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                               21.
C-TERMINAL DOMAIN.
EP-HAND [ POTENTIAL).
EF-HAND 2 (POTENTIAL).
                                                                                                                                                                                                                                                                                            MIDDLE DOMAIN.
                                                                                                                                                                                                                                                                                                            MC DOMAIN.
    EMBL; X14518; CAA32662.1; -. EMBL; X14519; CAA32663.1; ALL_SEQ. EMBL; X02593; CAB51571.1; ALL_SEQ.
                                                                                 InterPro, IFR002048; EF-hand.
InterPro; IPR001452; SH3
InterPro; IPR022017; Spectrin.
Pfam; PF00018; SH3; 1.
Pfam; PF00036; cfhand; 2.
                                                                                                                               PRINTS; PRO0452; SH3DOMAIN.
ProDom; PD000012; EF-hand; 1.
FroDom, PD000066; SH3; 1.
                                                                                                                          Pfam; PF00435; spectrin; 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 63.6
kgs 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                1845
11951
11951
12058
12477
12457
12452
                                                                                                                                                                                                                                                                                                                  167
                                                                                                                                                                                                                                                                                                                                                                                                                                             984
985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1024
                             A30122; SJCHA.
1SHG; 31-OCT-93.
                                                                   1TUD; 01-AUG-96.
                                                                            PDB; 18K2; 16-FEB-99.
                                             1AEY; 15-MAY-97
                                                   1AJ3; 07-JUL-97
1TUC; 01-AUG-96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2477 AM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            988
990
993
                                                                                                                                                                                                                                                                                                                                                                1740
                                                                                                                                                                                                                                                                                                                                                                                1952
2059
2172
                                                                                                                                                                                                                                                                                                                                                                                                                                             983
985
                                                                                                                                                                                                                                                                                                                                                                                                      2257
                                                                                                                                                                                                                                                                                                                  062
                                                                                                                                                                                                                                                                                                                                                                                                                      384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
CA_BIND
CA_BIND
                                                                                                                                                                                                                                                                                          DOMAIN
DOMAIN
DOMAIN
                                                                                                                                                                                                                                     REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                  REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                              STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAND
                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                 PEPEAT
                                                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rest Loca
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                             TURN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TUEN
                                     PDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOKN
                                                                   PDB;
```

. --.

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the SWISS institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute of There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license alterment (Suc http://www.isbrsit.chpatnoupurcy or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Them Riophys, Pes. Comman 274-666-674(1906)
FUNCTION: P-ACTIN CROSS-LINKING PROTEIN WHICH IS FROUGHT TO ANYBOR
ACTIN TO A VAPIETY OF "NIPACELLULAR STRUCTUPES, THIS IS A BURELING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Egerton M., Moritz R.L., Druker B., Kelso A., Simpson R.J., "Identification of the 70kD heat shock cognate protein (HSe70) and alpha-actinin-1 as novel phosphotyrosine-containing proteins in T
                                                                                                                                                                                 Homo sapiens (Human).
Fukaryota, Metaraa; Cherdata; Graniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                        AACT_HUMAN STANDAPD: PPT; 892 AA.
P12814.
01-0CT-1989 (Rcl. 12, Created)
01-0CT-1989 (Rcl. 12, Last sequence update)
16-0CT-2001 (Rcl. 40, Last annotation update)
Alpha-actinin 1 (Alpha-actinin cytoskeletal isctem) (Non-musclo-alpha-actinin 1) (F-actin pross linking protein).
                                                                                                                                                                                                                                                                                                                                                            MEDLINE-90274024; PubMed-2349951;
Youssoufian H., McAfee M., Kwiatkowski D.J.,
Youssoufian H., McAfee M., Kwiatkowski D.J.,
"Cleaing had The mesemal landary of the beta-spectrin gene.";
Am. I Hum Genet 47.62.74(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-90381709, Pubmed-2169343,
Nishiyama M., Ozturk M., Elohlich M., Mafun⊝ K.-I., Steele G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -:- SUBUNIT: HOMODIMER, ANTIPARALLEL.
-:- SIMILARITY: CONTAINS 1 ACTIN-HINDING DOMAIN.
-:- SIMILARITY: CONTAINS 2 CALFONIN-HOMOGEGY (CH) DEMAINS.
-:- SIMILARITY: CONTAINS 2 EF HAND CALCIM-BINDING DEMAINS.
-:- SIMILARITY: CONTAINS 4 SPECTRIN REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expression of human alpha actinin in human hepatoceilular
                                                                                                                                                                                                                                                                                         Millake D.B., Blanchard A.D., Patel B., Critchley D.R.; "The cDNA sequence of a human placental alpha-actinin."; Nucleic Acids Pes. 17:6725-6725(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro, IPR001589; Actbind_actnin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 134-146.
MEDLINE=96311348: PubMed-8713105;
                                                                                                                                                                                                                                                                              MEDLINE-8938599; PubMcd-2780298;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cander Res. 50:6291-6294(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 297 R92 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X15804; CAA33803.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL, M95178; AAA51582.1; ...
EMBL, X55187; CAA38970.1; -...
PTR, S05503; S05503.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HGNC:163: ACTN1.
        970 ELVLALYDYQE 980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSSP; Q01082; 18KR.
                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                           NCBI_TaxID-9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     lymphocytes."
Riochem Riop
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              carcinoma.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wands J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Genew;
```

```
This SWISS FROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Enteleostomi;
Mammalia; Eatheria; Kodentia; Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16-001-2001 (kel. 40, Created)
16-001-2001 (Pel. 40, Last argueure update)
16-007-2001 (Pel. 40, Last annotation update)
16-0072-2001 (Pel. 40, Last annotation update)
Alpha action ( Alpha action cytoskeletal isoform) (Non muscle alpha-action 1) (P-actio cross linking protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ċ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- SUBUNIT: HOMODIMER, ANTIPARALLEL (BY SIMILARITY).
-:- SIMILARITY: CONTAINS 1 ACTIN' BENDING DOMAIN.
-:- SIMILARITY: CONTAINS 2 CALPONIN'HOMOLOGY (CH) DOMAINS.
-:- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM'HINDING DOMAINS.
-:- SIMILARITY: CONTAINS 4 SPECTRIN REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63.6%, Score 35, DB 1, congth 892; 70.0%; Pred. No. 60;
                                                                                                                                                                                                                           PROSITE: PS99020; A.T.
PROSITE: PS90018; CH: 2.
PROSITE: PS00018; EF.HAND: 1.
Actin-binding: Calcium-binding: Repeat; Multigene family.
Actin-binding: 247 ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                 SPECTRIN 1.
SPECTRIN 2.
SPECTRIN 2.
SPECTRIN 4.
EF-HAND 1 (POTENTIAL).
R > L (IN REF. 3).
Q -> L (IN REF. 3).
G -> R (IN REF. 3).
G -> R (IN REF. 3).
T > L (IN REF. 3).
G -> R (IN REF. 3).
G -> R (IN REF. 3).
L -> F (IN REF. 3).
T > L (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismalches
InterPro, IPRGG1715, Calponin-like.
InterPro, IPRG02048, EF-hand.
InterPro, IPRG02017; Spectrin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            102974 MW:
                                                                                                                                              Promis PF00435; spectrin; 4. Probom; PD000012; EF-hand; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           70.08;
                                                                 Pfam; PF00036; efhand; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7; Concervative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                      Pfam; PF00307; CH; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 414 EAMLROKDYD 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ||SSOR-Hipporambus:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAC AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          i ELMLKLŲDYE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE PROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPONENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0921P2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTINI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC1_RAT
```

.. O

```
the European Hoinformatics Institute. There are no restrictions on its mase by inn-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and to, commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Castanon M.J., Hauplmann R., Wiche G.;
Junsual B. † Hanscript complexity of plectin isoforms: novel tissue-
specific exons modulate actin binding activity.";
Hum. Mol. Genet. 8:2461-2472(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cTPAIN CF7ML%1: TISSUE Pmbryc:
MEDLINE-21085660; FubMed-11217851;
Kawai J., Shinaqawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Melazoa; Chordata; Craniata; Vertebrata; Enteleostomi;
Mammalia; Eutheria; Rodentia; Sciuroqnathi; Muridae; Musinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FISSUR-Brain, Embryo, Heart, Kidney, Skeletal muscle, and Testis.
MEDLINE-20025755; PubMed-10556294;
Fuchs P., Zoerer M., Remaiczek G.A., Spazierer D., Ochler S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., ALHERNATIVE SPILICING, AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ΟΘΟΧΕΙ: ΟΘΟՄΙΣ, ΘΘΟΧΩΒ: ΩΘΟΧΩΘ: ΕΘΩΧΡΩ: ΘΘΟΧΡΙ: ΘΘΟΧΡΣ:
ΟΘΟΧΡΑ: ΟΘΟΧΡS: ΟΘΟΧΡS: ΘΘΟΧΡΑ: ΘΘΟΧΡΑ: ΘΘΟΧΡΑ: ΘΘΟΧΡΟ:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63.6%; Score 35; DB 1; Length 892; 70.0%; Pred. No. 60;
                                                                                                                                                                                                                                                                                                                          PROSITE; PSS0021; CH; 2.
PROSITE; PS00018; EF_HAND; 1.
Actin-binding; Calcium-binding; Repeat; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              102959 MW; 2360D496D0A84095 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EF-HAND 1 (POTENTIAL).

EF-HAND 2 (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16 OCT-2001 (Rel. 40, Last annotation update)
Plectin 1 (PLIN) (PCN) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT: 964 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1, Mismatches
                                                                                                                                                                                                                                                                                                                                                                          ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIRIN 2.
SPECIRIN 3.
SPECIRIN 4.
                                                            or send an email to license sish sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                       SPECTRIN 1.
                                                                                                                          InterPro; IPR001589; Actbind_actnin.
                                                                                                                                       InterPro; 1PR001715; Calponin-like.
InterPro; 1PR002048; EF hand.
                                                                                                                                                                                                                                                                             SMARI; SM00150; SPEC; Z.
PROSITE: PS00019; ACTININ_1; 1.
PROSITE; PS00020, ACTININ_2; 1.
                                                                                      EMBL; AF115386; AAD12064.1; -.
HSSP; Q01082; 18KR.
                                                                                                                                                                    InterPro: IPR002017; Spectrin
                                                                                                                                                                                                                  Ptam; PF00435; spectrin; 4.
Probom; PD000012; EF-hand; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 181-812 FROM N.A.
                                                                                                                                                                                      Ptam; PF00036; efband; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD:
                                                                                                                                                                                                                                               SMART; SM00033; CH; 2.
SMART; SM00054; EFb; 2.
                                                                                                                                                                                                                                                                                                                                                                                          <u>~</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus (Mouse).
                                                                                                                                                                                                      Pfam; PF00407; CH;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 892 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          414 EAMLROKDYE 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ELMLRLODYE 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                         144
274
394
509
630
759
800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  090365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PLE1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A HIND
                                                                                                                                                                                                                                                                                                                                                                                       NI VWOO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CA_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  090XS3;
                                                                                                                                                                                                                                                                                                                                                                          DOMA IN
                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLEC 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLE1_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hest
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its mass by non-profit institutions as load as its content is in no way modified and this statement is not recoved. Usage by and for commercial origins trajites a first article of (See M.F.) (Www lab all and recommercial origins).
A Arawa I., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., A Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Saito T., Gkazaki Y., Golobori T., Bono H., Kashawa T., Saito R., Radota K. Marsuda H.A., Saburner M., Batalov S., Casavant T., Kadota K., Marsuda H.A., Ashburner M., Batalov S., Casavant H., Ruchi P., Lewis S., Marsuo Y., Nikaido I., Pesole G., Quackenbush J., Schriml L.M., Staubi F., Suzuki R., Tomita M., Waqner I., Washio I., Sakai K., Okido T., Furuno M., Aono H., Baidarelli R., Barsh G., Braka K., Okido T., Furuno M., Aono H., Baidarelli R., Barsh G., Brownstein M.J., Bult C., Fletcher C., Fujita M., Garibodi M., Gristincich S., Hill D., Holmann M., Hume P.A., Kamiya M., Ler N.H., Austrincich S., Hill D., Holmann M., Hume P.A., Kamiya M., Ler N.H., Austrincich S., Hill D., Holmann M., Mordone C., Sakamicho N., Sakamicho N., Sakamicho N., Sakamicho N., Sakamich M., Storch A.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Na ususaki M., Storch A., Sasaki H., Saku K., Schochbach C., Seya I., Shibata Y., Storch A., Suzuki H., Toyo-oka K., Wang K., Haseqawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MICROFILAMENTS. AND ANY DESCRIPTION OF THE ANY OF THE METAL OF THE MET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LUNG, BRAIN, SMALL INTESTINE, MUSCLE, HEART AND SKIN WITH LOWER LEVELS FOUND IN KIDNEY, LIVER, UTERGS, SPLEEN AND SALIVARY GLAND.
-i- DOMAIN: THE N-TERMINUS INTERACTS WITH ACTIN, THE C-TERMINUS WITH VIMENTIN, DESMIN, GFAD, CYTOKERATINS, LAMIN B: WHEREAS ROTH THE N-AND THE C-TERMINUS CAN BIND INTEGRIN BETA-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H- FUNCTION: INTERLINKS INTERMEDIATE FILAMENTS WITH MICROTURBLES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to licenseaisb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, AF188013; AAF18073.11
EMBL, AF188014; AAF18074.11
EMBL, AF188015; AAF18076.11
EMBL, AF188016; AAF18076.11
EMBL, AF188017; AAF18078.11
EMBL, AF188019; AAF18079.11
EMBL, AF188020; AAF188011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF188006; AAF18066.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HMBL; AF188021; AAF18081.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAF18067.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF188007;
```

BAB 10907.1; ALT\_INIT.

EMBL, AF188022; AAF18082.1; -. EMBL; AF188023; AAF18083.1; -.

InterPro; PR001589; Actbind\_actnin. InterPro; IPR001715; Calponin-like.

Flec1

MGD, MGI.1277961,

EMBL; AK017743;

```
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISSING (IN ISOFORM PLECTH).
MISSING (IN ISOFORM PLECTH).
MISSING (IN ISOFORM PLECTH).
MISSING (IN ISOFORM PLECTE).
MISSING (IN ISOFORM PLECTE).
MISSING (IN ISOFORM PLECTH).
                                                                                                                                                                                                                                                                                                                                                       MEPSGSLEPSLVVVGHVVTLAAVWHWRKGHRQAKDEO (IN ISOPORM PLEC-16 AND ISOPORM PLEC-18, 2A) MVAGMI.MPLDRLRAIYEVLEREGVWVAKKDRRPRSLHPHVP
                                                                                                                                                                                                                                                                                                                                                                                                                              GVTNLQVMRAMASLKARGLVRETFA -> MSGEDSEVRPVA
VAEGSSNGSSGSPSPGDTLPWNLGKTQPSPRSGGGSVGNGS,
                                                                                                                                                                                                                                              MVACMIMPIDHIRATYEVIPRESVMVAK > MAHILITSOD
PPDEQDETQAYEEVREKYK (IN ISOFORM PLEC-1F).
MVACMIMPIDRIRATYEVIFREGVMVAKKDRRP -> MNET
                                                                                                                                                                                                                                                                                VCPPKLSPSGSTNTLSPLFGTSVTGTKTS (IN ISOFOPM
                                                                                                                                                                                                                                                                                                                                                                                                       GYLYGQICCV (IN ISOFORM PLEC-1G).
MVAGMIMPIDRLRALYEVLFREGVMVAKKDRRPRSI.HPHVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MISSING (IN ISOFORM FLECT), 130FORM PLECTA, ISOFORM PLECTID, ISOFORM PLECTIC, ISOFORM PLECTIC, ISOFORM
                                                                                                                                                                                                                                                                                                                    MSQHRI.RVPEPEGI.GSKRTSSEDNI.YI.AVI.RASEGKK (IN
                                                                                                                                                                                                                                                                                                                                                                                             GVT -> MAGTWAAKGVFTSQREVILLERPCWLDGGCEQVRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                    VEDPAEPAVIFIA (IN ISOFORM PLEC-6, 10, 10, 1SOFORM PLEC-0, 1C, 2A, 3A AND ISOFORM PLEC-
                                                                                                                                                                                                                                                                                                         MVAGMIMPLDPLPATYEVLFPEGVMVAKKDRRPRSLH ->
                                                                                                                                                                                                                                                                                                                                             MVACMIJMPT.DRIJRATYEVIJEREGVMVAKKIDRRPRST.H ->
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                 ISOFORM PLEC-1E AND ISOFORM PLEC-1E,2A)
                                                                                                                                                         SPECTRIN 1.
SPECTRIN 2.
SPECTRIN 2.
MAGM -> MKIVP (IN ISOFORM PLEC 1D AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLEC-1F, ISOFORM PLEC-0,10 AND ISOFOPM PLEC-1B).
                                                                                                                                                                                                                     MEPSEALQHEISSLK (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> ERDVIRSVRIJPRI (IN ISOFORM FLEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 35; DB 1; Length 964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3; indels
                                                                                   protein: Cytoskeleton: Actin-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111661 MW: 1E2846BF2B72A30E CPM64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E -> ERDVIRSVRLAMED (
0,1C,2A,3A).
MISSING (IN REF. 2).
                                                                                                                                                                                                          ISOFORM PLEC-1D, 2A).
                                                                                                                                                                                                                      MVAGMIMPLDRLEAI ··
                                                                                                                                                                                                                                                                                                                                 ISOFORM PLEC-1A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1; Mismatches
                                                                                                                       ACTIN-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 65;
      InterPro; IPR002017; Spectrin.
Pfam; PF03107; CH; 2.
Pfam; PF04501; SIQ_Picetin. 1
PROSITE; PS00019; ACTININ_1; 1
PROSITE; PS00020; ACTININ_2; FALSE_NEG.
                                                                                                            CLORULAR
                                                                                                                                                                                                                                                                                               PLEC-11)
InterPro: IPROA5326: Slo_plectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity 63.6 es 7, Conservative
                                                                                                                                                                                                                     15
                                                                                                                                                                                                                                            28
                                                                                                                                                                                                                                                                  33
                                                                                                                                                                                                                                                                                                         33
                                                                                                                                                                                                                                                                                                                                             37
                                                                                                                                                                                                                                                                                                                                                                                44
                                                                                                                                                                                                                                                                                                                                                                                                                    99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
180
180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       180
180
                                                                                            Alternative splicing.
DOMAIN 1 >96
DOMAIN 181 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       964 M
                                                                                 Repeat: Structural
                                                                                                                      181
185
306
653
748
845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16
23
34
38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARSPLIC
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VARSPLIC
VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VARSPLIC
VARSPLIC
                                                                                                                                                                                              VARSPLIC
                                                                                                                                                                                                                                            VAPSPLIC
                                                                                                                                                                                                                                                                                                                                             VARSP1.1C
                                                                                                                                                                                                                                                                                                                                                                                                                  VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARSPI.IC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFILICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SECTIENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                     VARSPLIC
                                                                                                                                                                                                                                                                     VARSP1.1C
                                                                                                                                                                                                                                                                                                         VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARSP1.1C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARSPLIC
                                                                                                                                DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NON TER
                                                                                                                                                          REPEAT
                                                                                                                                                                      REPEAL
                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hest
```

```
1 ELMLRLQDYEE 11
```

PLE1\_CRIGR RESULT 12

|| || || || || 424 || ELOLRWQEYRE 434

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are not restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/of send an enail to licensealsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                  - DOMAIN: THE N-TERMINUS UTDERACTS WITH ACTIN, THE C-TERMINUS WITH VIMENTIN, DESMIN, GFAP, CYTOKERATINS, LAMIN B; WHEREAS BOTH THE N-THE C-TERMINUS CAN BIND INTEGRIN BETA-4.

- PEW PHOSPHORYLATED BY CTC2, PEGILATES FISSCIATION FROM INTERMEDIATE FILAMENTS DURING MITOSIS.

- SIMILARITY: CONTAINS 1 ACTIN HINDING DOMAIN.

- SIMILARITY: CONTAINS 2 CALDONIN-HOMOLOGY (CH) DOMAINS.

- SIMILARITY: CONTAINS 3 PLECTIN REPEATS.

- SIMILARITY: CONTAINS 4 SPECTRIN PEPEATS.
                                                                                                                                                                                                                                    Clubb B.H., Chou Y.-H., Herrmann H., Svitkina F.M., Horisy G.G., Goldman R.D., The Soldman R.D., The 30G-Kbainternediate lilament associated protein (IfAP300) is a Hamster plectin ortholog.", Highlys Res Commun, 273:183-187(2009).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Coiled coil: Repeat; Structural protein; Cytoskeleton: Actin-binding;
                                                                                                                              Edkaryota, Mota⊼od, Chotdata, Craniata, Vertebrata, Euteleostomi;
Mammalia: Eutheria; Rodentia; Sciurognathi; Muridae; Cricetinae;
                                           16 CCT-2001 (Rel. 40, Läst sequence update)
16 OCT-2001 (Rel. 40, Last annotation update)
Plectin I (PLIN) (PCN) (300-kDa intermediate filament-associated
                                                                                                                                                                                                                                                                                                                                        MEDITINESSECTIONS: PubMed M626512; Malecz N., Folsner R., Stadler C., Wiche G.; Tdentification of plectin as a substrate of p34cdc2 kinase and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CENTRAL FIBROUS ROD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLOBULAR 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLOBULAR 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPOSITE: PS00020; ACTININ_2; FALSE_NEG. PPOSITE: PS50021; CH: 2.
                                                                                                                   Cricetulus griseus (Chinese hamster).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPP001589; Actbind_actnin.
InterPro; IPR001715, Calponin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001101; Plectin_repeat.
                                                                                                                                                                                                                          MEDLINE-20334248; PubMcd-10873583;
                             16-0CT-2001 (Rel. 40, Created)
                                                                                      protein) (iFAP300) (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF260753; AAF70372.1; -
 STANDARD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1259
2544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP; Q01082; 1BKR
                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                             NCB1_TaxID-10029;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <1
1260
                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphorylation.
                                                                                                                                                               Cricetulus.
PLELCRIGE
Q9JI55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
DOMAIN
DOMAIN
                                                                                                  PLEC1
```

```
"Human plectin: organization of the gene, sequence analysis, and chromosome localization (8q24).";
Froe. Nati. Acad. Sci. U.S.A. §38:4278-4283(1996).
                                                                                                SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), AND DISEASE.
                                                                                                                                                                                                                                                              qenomic organization.";
                                                                                                                                                                                                                                                                                                                          VARIANT MD-EBS 1003-GLN--ALA-1005 DEL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   muscular dystrophy.";
Hum. Mol. Genet. 5:1539-1546(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-21090821; PubMed-11159198;
                                                                                                                        MEDILINE-96312447; PubMcd-8698233;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL, 254367, CAA91196.1; -.
EMBL, U53204, AAB05427.1; -.
EMBL, U634519, AAB05428.1; -.
EMBL, U634609, AAB05428.1; -.
EMBL, X97033; CAA65765.1; -.
HSSP; Q01082; 1HKR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J. Pathol. 158:617 625(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wiche G., Uitto J., Hintner H.;
                                                                                                                                                                                                                                                                                  Jenes Dev. 10:1724 1735(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VARIANT MD-EBS LEU-429 INS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HGNC:9069; PLEC1
                                                                                                                                                                                                                                                            CDNA cloning and
                                                                                                                                                                                                                 Uitto J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genew;
         0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BINDING TO INTERMEDIATE FILAMENTS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa: Chordata: Craniata: Vertebrata; Eureleostomi;
Mammalia: Eutheria; Primates: Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29 4 X 4 AA IÁNDEM REDEATS OF G-S-R-X.
28 FPGSFPGKYLAFTON (BY CDC2).
509015 MW; E144615D361E3484 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-96210632; PubMed-8633055;
Liu C.-G., Macreker C., Castanon M.J., Hauptmann R., Wiche G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 4473;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PiEl_HDMAN STANDARD; PRI; 4684 AA. 015149: 015449: 015449: 045440: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045449: 045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                            COLLED COIL (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63.6%; Score 35; DB 1; I
63.6%; Pred, No. 3.6e<sup>1</sup>02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Mismatches
  ACTIN-BINDING
                                                                   SPECTKIN 1.
SPECTKIN 2.
SPECIKIN 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       237 .
                                                                                                                                         SPECIRIN 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLECTIN 23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY)
                                                                                                                                                                                                                                                                                                                                           PLECTIN 8.
PLECTIN 9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLECTIN 31
                                                                                                                                                                                      PLECTIN 1.
                                                                                                                                                                                                                                                                                                     PLECTIN 6.
                                                                                                                                                                                                            PLECTIN PLECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PLECTIN DELECTIN DELECTIN DELECTIN DELECTIN DELECTIN DELECTIN DELECTION DELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PLECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLECTIN
PLECTIN
                                                                                                                                                                                                                                                                             PURCHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLECTIN
                                                                                                                                                                                                                                                                                                                          PLECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                 PLECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                         PLECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NITORIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MILOHIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NILECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NI LECT IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SECUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Conservative
                                                                                                                                                                                                                                                                                                                                              3018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3722
                                           283
508
                                                                                                                                                                                                                                                                          2804
                                                                                                                                                                                                                                                                                                                                                                                                                                                          3487
3425
3463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3646
                                                                                                                                                                                    2652
                                                                                                                                                                                                                                                                                                                          2980
                                                                                                                                                                                                                                                                                                                                                                                                                                       3344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4.428
                                                                                                                                                                                                                                                                                                                                                                                           3094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      788t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34.57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5961
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   43864089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1041
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               205 ELULRWQEYRE 215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4473 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ELMLRLQDYEE 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_FaxID 9606;
                                                                                                                                      1104
1258
2615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rissue placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3647
3685
3723
4764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            $800
$852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      47.5H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4043
                                                                                                                                                                                                                                                                                                  3405
                                                                                                                                                                                                                                                                                                                                                                      1019
                                                                                                                                                                                                                                                                                                                                                                                                                 1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                            150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4966
                                                                                                                                                                                                                                                                                                                          2.14 3
                                                                                                                                                                                                                                                                                                                                              3981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
DOMAIN
DOMAIN
BOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOD RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
REPEAT
                                                                                                                                                            DOMA!N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DOMA I N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                           REPEAT
                                                                                                                REPEAT
                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                             REPEAL
                                                                                                                                                                                                                                                                                                  REPEAL
                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KELPEA I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                         REPEAL
                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                              REPEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                         REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PLEC1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLET HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hess t
```

```
MICROFILAMENTS AND ANCHORS INTERMEDIATE FILAMENTS TO DESMOSORES OR HEMIDESMOSOMES. COULD ALSO BIND MUSCLE PROTEINS SUCH AS ACTIN TO MEMBERARE COMPLEASES IN MUSCLE. MAY BE INVOIVED NOT ONLY IN THE CROSSILINKING AND STAHLIZATION OF CYTOSRELETAL INTERMEDIATE FILAMENTS INTERMEDIATE.

-1. SUBBUILT: HOMODIMER OR HOMOTETRAMER.
-1. ALTERNATIVE PRODUCTS: 3 ISOPORMS; I (SHOWN HERE), 2 AND 3; ARE PRODUCED BY ALTERNATIVE SPLICING.
-1. ISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST LEVELS IN MUSCLE, HART, PLACKENTA AND SPINAL. CORD.
-1. DOMAIN: THE N-1EMENAUS INTERACTS WITH ACTIN, THE C-TERMINUS WITH VIMENTIN, DESMIN, GRAP, CYTOKERATINS, LAMIN B; WHEREAS BOTH THE N-YIMENTIN, DESMIN, GRAP, CYTOKERATINS, LAMIN B; WHEREAS BOTH THE N-AND THE C-TERMINUS MITH VIMENTIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. Usage by and for commercial entitles requires a liceuse agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the Swiss Institute of Bioinformatics and the EMML outstation the Endepean Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-97049959; PubMed-8894687; Pulkkinen L., Smith F.J.D., Shimizu H., Murata S., Yaoita H., Hackisuka H., Nishikawa T., Melcan W.-H., Uitto J., "Homozygous deletion mutations in the pleetin gene (PLECI) in patients with epidermolysis bullosa simplex associated with lateronsed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "A compound heteroxygous one aminorabid insertion/consecute mutation in
the plectin gene causes epidermolysis buliosa simplex with plectin
deficiency.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WITH MOSCULAR DYSTROPHY (MD-ERS OR EH-MD), AN AUTOSOMAL RECESSIVE DISORDER CHARACTERIZED BY EPIDERMAL RISSTER FORMATION AT THE LEVEL OF THE HEMIDESMOSOME AND ASSOCIATED LATE-ONSET MUSCULAR DYSTROPHY.
SIMILARITY: CONTAINS 1 ACTIN-BINDING DOMAIN.
SIMILARITY: CONTAINS 2 CALFONIN-HOWGLOCY (CH) DOMAINS.
SIMILARITY: CONTAINS 3 PILECTIN REPEATS.
SIMILARITY: CONTAINS 3 PILECTIN REPEATS.
SIMILARITY: BELONGS TO THE PLAKIN OR CYTOLINKER FAMILY.
                                                                                                                                                                                                                      Loss of plentin causes epidermolysis bullosa with muscular dystrophy:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ! FUNCTION: INTERLINKS INTERMEDIATE FILAMENTS WITH MICHOLUBULES AND
McLean W.H.I., Pulkkinen L., Smith F.J.D., Rudg E.L., Lane E.B.,
Bullrich F., Burgeson R.E., Amano S., Hudson D.L., Owaribe K.,
McGrath J.A., McMillan J.R., Eady R.A.J., Leigh I.M., Christiano A.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISHASE: DEFECTS IN PLECT ARE THE CAUSE OF EPIDERMOLYSIS HULLOSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bauer J.W., Rouah F., Kotier B., Rezniczek G.A., Kornacker I.,
Muss W., Hamether R., Klausegger A., Buber A., Pohlardubo G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PTM - PHOSPHOPYLATED BY CLOZE, REGULATES DISSOCIATION FROM INTERMEDIATE FILAMENTS DURING MITOSIS (BY SIMILARITY).
```

```
321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [2]
PEVISIONS.
                                                                                                                                                                                                                                                 CONFLICT
CONFLICT
CONFLICT
CONFLICT
                                                                                                                                           CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
CONFLICT
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CONFLICT
                                     VARSPLIC
                                                                                                                                                                                                  CONFLICT
                                                                                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                      VAR! ANT
                                                                                        VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLE1_RAT
 GVTNLQVMRAMASLRARGLVRETEAWCHFFWYLTNEGTAHL.
ROYTHILPBELYAASLIQRVRRYVAWWHARRTPHVQAVQGPL,
GSPPREDLYASPLOLLYPRELEEVSPETPVVPATTGPTLA
RPGPEPAPAT -> MSSFPARFVAELEVSNSSSSSSSPSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MVACMUMPRDQL/RATYEVL/FREGVMVAKKDRRPRSL/HPHVP
                                                                                                                                                                                                                                                                                     Colled coil) Repeat. Structural protein; Cytoskeleton; Actin-binding;
Phosphorylation; Alternative splicing, Epidermalysis bullosa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BINDING TO INTERMEDIATE FILAMENIS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
4 X 4 AA TANDEM PEPEATS OF G-S-R-X.
PHOSPHORYLAIION (BY CDC2) (BY
                                                                                                                                                                                                                                                                                                                                                            CENTRAL FIBROUS ROD DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIFIN 4.
COLLED COLL (POTENTIAL).
PLECTIN 1.
                                                                                                                                                                                                                                                                                                                                                                                              ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECTRIN 1
SPECTRIN 2
SPECTRIN 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLECTIN 11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLECTIN 4.
PLECTIN 5.
PLECTIN 6.
PLECTIN 7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PLECTIN 9.
PLECTIN 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLECTIN 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLECTIN 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PLECTIN 33
                                                                                                                                                                                                                                                                                                                                                                             GLOBULAR 2
                                                                                                                                                                                                                              PROSITE: PS00019; ACTININ_1; FALSE_NEG-PROSITE; PS00020; ACTININ_2; FALSE_NEG.
             MIM; 226573;
InterPro; (PR001589; Actbind_actnin.
InterPro; (PR001715; Calpenin.like.
InterPro; (PR001101; Plectin_repeat.
InterPro; (PR002017; Spectrin.
Plam: PP00407; CH: 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PLECTIN 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PLECTIN 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLECTIN 1
PLECTIN 1
PLECTIN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLECTIN 1
PLECTIN 1
PLECTIN 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLECTIN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PLECTIN 2
PLECTIN 2
PLECTIN 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PLECTIN PLECTI
                                                                                                                                                                                                                                                                                                                                           GLOBULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PLECTIN
PLECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLECT IN
                                                                                                                                     Pfam; PF00681; Ploctin; 19
Ptam; PF03501; S10_plectin; 1;
SMART; SM000250; PLEC; 33;
SMART; SM00150; PLEC; 33.
                                                                                                                                                                                                                                                                    PROSITE; PS50021; CH; 2
                                                                                                                                                                                                                                                                                                                                         1470
2755
4684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1415
12863
12863
12863
12863
12863
13153
13154
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
13164
1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4100
4138
4176
4214
4252
4305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4445
4483
4521
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4559
4597
4300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3857
3895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174
                                                                                                                                                                                                                                                                                                                     Disease mutation
DOWAIN
1471
DOWAIN
1471
DOWAIN
175
DOWAIN
179
DOWAIN
179
REPEAT
REPEAT
740
                                                                                                                                                                                                                                                                                                                                                                                            175
179
295
645
740
837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2940
2981
3116
3154
3192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3268
3306
3485
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3820
3858
3896
3934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4139
4177
4228
4265
4319
4408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4063
4101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOD_PES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
DOMAIN
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
PEPFAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PEPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
PEPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMA I N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PEPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REPEAT
```

```
TLPWNLGKIÇRSRRS:333A3SNGSVLDPAERAVIRIA (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wiche G., Becker B., Luber K., Weitzer G., Castanon M.J.,
Hauptmann R., Stratowa C., Stewart M.;
"Cloning and Sequencing of rat plectin indicates a 466-kD polypeptide chain with a three-domain structure based on a central alpha-helical G. Cell Biol. 114:83-99(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hakarycta, Mčtavsa, Cbórdata, Chaniata, Vertebrata, Hateleostomi,
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 4684;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3; Indels
           ISOFORM 2 AND ISOFORM 3). MISSING (IN ISOFORM 3).
                                                                                                                                                                                                                                   <u>:</u>
                                                        MISSING (IN MD-EBS).
/FIG-VAR 01137.
S -> F (IN NEF. 2).
N -> D (IN NEF. 2).
H -> N (IN NEF. 2).
                                                                             -> F (IN REF. 2).
-> D (IN REF. 2).
-> D (IN REF. 2).
                                                                                                                                                                                                                                  (IN REF.
                                    L :> LL (IN MD-EBS).
/FTId=VAR_011336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DH 1; I
Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1993 (Rcl. 25, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                         KEF.
                                                                                                                                                                                                                                                                                                                                              REF.
                                                                                                                                                                                                                                                                                                                      RIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT; 4687 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 1).
FISSUE-Glial tumor;
MEDLINE-91268156; PubMed-2050743;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PLE1_RAT STANDARD; PH
P30427; 008879; 008880; 008881;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.68;
63.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ouery Match
Hest Local Similarity 63.0.
7, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rattus norvegieus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plectin i (PLIN) (PCN).
PLBC1.
                                                                                                                                                                                              23.24
20.24
20.24
20.24
20.24
20.24
20.24
20.24
20.24
20.24
                                                                                                                                                                                                                                                                                                                                                        3361
3447
3531
3531
3580
3580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              413 ELQUEWQEYRE 423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ELMLRLQDYEE 11
                                                                                                                                                                                                                                                                                                                                                                                             3531
3580
3589
                                                                                                                                                                                                                     662
688
767
                                                                                                                                                                                                                                                          1789
```

```
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss institute of Ricinformatics and the BMH contraction the European Alcinformatics lastitute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See hith plane is to commercial or send an email to licenseatish-sib.ch).
                                                                                                                                                                                                                                                    "Plectin transcript diversity: identification and tissue distribution of variants with distribute.

Our variants with distribut lirst coding exons and rodless isolorms.";

Ocnomics 42:115-125(1997)

I FUNCTION: INTERLINKS INTERMEDIATE FILAMENTS WITH MICROTHUMES AND MICROFILAMENTS AND MICROFILAMENTS TO DESMOSOMES. ON HENDIESWISOBES. MAY BE INVOIVED NOT ONLY IN THE CROSSLINKING AND STABILIZATION OF CYTOSKELETAL INTERMEDIATE FILAMENTS NETWORK, BUT ALSO IN THE REGISTATION OF THEIR POYAMICS.

I SUBJUIL: HORODIMES OF REMOTERRAMER.

I ALTERNATIVE PRODUCTS: 4 ISOFORMS; 1 (SHOWN HERE), 2, 3 AND 4; ARE PRODUCTS BY ALLERNATIVE SPECIFICANCE.

SKELFTAL MISCLE AND LOWEST IN THEMES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    I- DOMAIN: THE N-TERMINDS INTERACTS WITH ACTIN, THE C-TERMINDS WITH VIMENTIN, DESMIN, GFAP, CYTOKERATINS, LAMIN B; WHEREAS BOTH THE N-AND THE C-TERMINDS CAN BIDD INTEGRIN BETA-4.
I- PTM: PHOSPHORYLETED BY CDC2; REQUIRETES DISSOCIATION FROM INTEREDIATE FILAMENTS DOMENO MYTOSIS (BY SIMILARITY: CONTAINS I ACTIN-BINDING DOMAIN.
I- SIMILARITY: CONTAINS I ACTIN-BINDING DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Colled coil; Repeal, Structural protein; Cytoskeleton; Actin-binding;
Phosphorylation; Alternative splicing.
DOMAIN 1473 GLOBOLAR 1.
                                                                                                                                                   PARTIAL SEQUENCE FROM N A (ISOFOPMS 2: 3: 4), AND TISSUE SPECIFICITY
                                      Liu C.-G., Macreker C., Castanon M.J., Hauptmann R., Wiche G.; "Human pleetin organization of the yene, sequence analysis, and chromosome localization (8q24).";
Proc. Natl. Acad. Sci. U.S.A. 93:4278-4283(1996).
                                                                                                                                                                                         MEDLINE 97421050; PubMed-9177781;
Elliott C.E., Becker B., Ochler S., Castanon M.J., Hauptmann R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: BELONGS TO THE PLAKIN OR CYTOLINKER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CENTRAL FIRRGUS ROD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 - CAUTION: ISOFORM 4 IS A FPACMENT AT THE N-TEPMINHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY: CONTAINS 33 PLECTIN REPEATS. SIMILARITY: CONTAINS 4 SPECIFIN PEPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLOBULAR 2.
ACTIN-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSTIE: PSO0019, ACTININ, PEAUSE NET PROSTIE; PSO0020; ACTININ 2; FALSE_NEG. PROSTIE; PS50021; CH; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro, IPR001589; Actbind actnin.
InterPro, IPR001715; Calponin-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001101; Plectin_repeat.
InterPro; IPR005326; S10_plectin.
InterPro; IPR002017; Spectrin.
                    MEDIJINE-96210642; PubMed-R644055;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pram. PF00407, CH. 2.
Pram. PF00407, CH. 2.
Pram. PF004501, SIO_plectin; 1.
SMART: SM00043, CH. 2.
SMART: SM00250; PLEC; 3.
SMART: SM00150; SPEC; 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL: X59601; CAA42169.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, 096274; AAC53209.1; ...
EMBL, 096275; AAC53210.1; -..
EMBL, 096276; AAC53211.1; -..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4687
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIR; A39638; A39638.
PIR; S21876; S21876.
HSSP; Q01082; 18KR.
                                                                                                                                                                         IISSUE-Glial tumor;
TISSUE Glial tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1474
2759
181
185
                                                                                                                                                                                                                                         Wiche G.:
```

```
::
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RQYLHLPPETVPASLQRVRRPVAMVMPARKRSPHVUTMGP
LGCPPKRGPLPAEDPAREERQVYRRKEREEGAPETPVVSAT
IVGTLARPGPEPTPAT -> MEPSGSLFPSLVVGHVVSLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GVTNI, QVMRAATSI, KARGI, VRETFAWFHFYWYI, TNEGTIDHI.
RQYI, HI, PPET I VPASI, QRVRRPVAMVMIPARKRSPHVGT MQQP
LGCPPRRPQFI, PAEUPAREERQVYRKEIFEGAPET PVVSAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IVGTLARPGPEPTPAT -> MSQQRLRVPEPEGLGSKRTSS
EDNLYLAVLRASEGKK (IN ISOFORM 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AVWHWRKGHRQAQDEQ (IN ISOFORM 3).
MVAGMI.MPI.DQI.RATYEVI.FYEGVMVAKKDRRPRSI.HPHVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IVGTLARPGPETPAT -> DVSNGSSGSPSPGDTLPWNLG
KTQRSRRSGGGSVGNGSVLDPAERAVIRIA (IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MVAGMIJMPIJDQLIRATYEVIJEREGVMVAKKDRRPRSIJHPHVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ROYLHLPPETVPASLORVRRPVAMVMPARRRSPHVGTMUGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LGCPPKRGPLPAEDPAREERQVYPRKEREEGAPETPVVSAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MVAGMIJMPIJIQLKA LYEVLJE KEGVMVAKKIJKRPRSIJHPHVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GVTNLQVMRAMTSLKARGLVRELFAWCHFYWYLTNEGTDH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GVTNLQVMRAMTSLKARGLVRETFAWCHFYWYLTNEG1DHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                            4 X 4 AA TANDEM REPEATS OF G-S-R-X FHOSFHORYLATION (BY CDC2) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :.
=
                                                                                                                                                                                                                                                                                                                                                                                                                                                    BINDING TO INTERMEDIATE FILAMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 4687:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9966CAF71H929751 CRC64;
                                             COILED COIL (POTENTIAL)
COILED COIL (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 35; DB 1; I
Pred. No. 3.8e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
 SPECTRIN 1.
SPECTRIN 2.
SPECTRIN 3.
SPECTRIN 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                       PLECTIN 33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFORM 4)
                                                                                                      PLECTIN
                                                                                                                                                                                   PLECTIN
PLECTIN
PLECTIN
                                                                                                                                                                                                                                                      PLECTIN
PLECTIN
                                                                                                                                                                                                                                                                                                                                    PLECTIN
PLECTIN
                                                                                                                                                                                                                                                                                                                                                                     PLECT IN
                                                                                                                                                                                                                                                                                                                                                                                          PLECTIN
PLECTIN
PLECTIN
                                                                     PLECTIN
                                                                                                                                      PLECTIN
                                                                                                                                                                                                                                                                                                             PLECTIN
                                                                               PLECTIN
                                                                                            PLECTIN
                                                                                                                             PLECTIN
                                                                                                                                                   PLECT IN
                                                                                                                                                              PLECTIN
                                                                                                                                                                          PLECTIN
                                                                                                                                                                                                                       PLECT IN
                                                                                                                                                                                                                              PLECTIN
                                                                                                                                                                                                                                            PLECT IN
                                                                                                                                                                                                                                                                             PLECTIN
                                                                                                                                                                                                                                                                                        PLECTIN
                                                                                                                                                                                                                                                                                                    PLECTIN
                                                                                                                                                                                                                                                                                                                         PLECTIN
                                                                                                                                                                                                                                                                                                                                                           PLECT IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE 4687 AA; 533527 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ouery Match
Best Local Similarity 63.6
Matches 7: Conservative
                                                                                                                                                                                                                                                                                     3936
                                                                    2828
2866
2904
2942
2980
                                                                                                                                                                                                       355.5
356.3
360.1
                                                                                                                                                                                                                                           3639
                                                                                                                                                                                                                                                                3860
                                                                                                                                                                                                                                                                                                                                                                                                     4486
4524
4562
4600
4303
                                                                                                                                                             3232
3270
3308
                                                                                                                                                                                                                                                                                                             4011
4103
4141
4179
4217
                                                                                                                                                                                                                                                                            868
                                                                                                                                                                                                                                                                                                                                                                     255
308
448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       419 ELQLRWQEYRE 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ELMLRLQDYEE 11
                                                                                                                                      3119
3157
3195
                                                                                                                                                                                                                    3526
3564
3602
                                                                                                                                                                                                                                                     3643
3823
3861
                                                                                                                                                                                                                                                                                                                                              4142
4180
4221
4258
                                                                                                                                                                                                                                                                                                                                                                                                     4449
                                                                               2829
2867
2905
2943
2984
                                                                                                                                                                                               3311
                                                                                                                                                                                                                                                                                                                       4066
                                                                                                                                                                                                                                                                                       6688
                                                                                                                                                                                                                                                                                                   1937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VARSP1.1C
                                                                                                                                                                                                                                                                                                                                                                                                                                    KEPEAT
DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M.C.RES
                                                                           REPEAT
                                                                                                                                                                                                                                                     REPEAT
REPEAT
                      REPEAT
REPEAT
                                                                                                      REPEAT
REPEAT
                                                                                                                                                                                              REPEAT
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
REPEAT
REPEAT
REPEAT
                                                                                                                                                                                                                               REPEAL
                                              DOMAIN
                                                          DOMAIN
                                                                                                                                                                                                                                                                                                   REPEAT
                                                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                     REPEAT
                                                                                            REPEAT
                                                                                                                                       REPEAT
                                                                                                                                                   REPEAT
                                                                                                                                                              PEPEAT
                                                                                                                                                                        REPEAT
                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                            REPEAL
                                                                                                                                                                                                                                                                             REPEAT
                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                        REPEAT
                                                                                                                                                                                                                                                                                                                                    REPEAT
                                                                                                                                                                                                                                                                                                                                               REPEAT
                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                      REPEAT
                                                                                                                                                                                                                                                                                                                                                                               PPPPAT
                                                                                                                                                                                                                                                                                                                                                                                            REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                             REPEAT
```

```
This SWISS-PROI entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the EMUCOPAN BIOINFORMATICS Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                        Eukaryóta, Viridiplantae, Streptophyta, Embryophyta; Tracheophyta;
Spermatophyta, Maduoliophyta, Liliopsida; Foales; Poaceae; PACC clade;
Panicoldeae; Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-92096457; PubMed-1756176; Dobrowolska G , Roldyretf B., Issinger O.-G.; "Cloning and sequencing of the casein kinase 2 alpha subunit from Zea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cascin kinase II, alpha chain (CK II) (EC 2.7.1.37) (CK2-alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transterase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61.8%; Score 34; DB 1; Length 332; 60.0%; Pred. No. 31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            39230 MW; 85513A5A5C77235A CRC64;
                            332 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochim. Biophys. Acta 1129:139-140(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to licensewish-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSLIE; PS00107; PROTEIN_KINASE_ATP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE: PS00108; PROTEIN_KINASE_ST: 1.
PROSITE: PS50011; PROTEIN_KINASE_DOM: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matricia, συντά.
InterPro, 1PR002290; Buk_pkinase.
InterPro, 1PR002290; Ser thr_pkinase.
FrancoponAct. okinase: I.
                            PRI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euk_pkinase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL: x61387; CAA43659.1; -.
                         STANDAED,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48
63
151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Probom; Phododol; Euk_p
SMART; SM00220; S_TKC;
                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-cv. B73 Inbred:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; $16387; $16387.
; $19726; $19726.
; 1LR4; 29-MAY-02.
zedb; 30032; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 34 3
40
63
151 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
es 6, Conserv
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CK2 SUBFAMILY
                                                                                                                                                                                                                    Sea mays (Maize).
                                                                                                                                                                                                                                                                                                                    NCB1_Tax1D-4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3D-structure.
                         KC2A_MAICE
P28523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MaizeDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ON H dN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
KC2A_MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR;
PDB;
                                                  STITIMEN AND SECOND TO THE PROPERTY OF SECOND SECOND TO THE PROPERTY OF SECOND SECOND
```

ó

0; Gaps

1; indels

Mismatches

3.

Conservative

Matches

1 ELMLRLQDYE 10

ò

```
196 ELLVDLQDYD 205
```

q

Scatch completed, January 16, 2003, 16.5).14 Job time : 17.0286 secs

